

SEQUENCE LISTING

<110> Hallahan, David L.

<120> cis-Prenyltransferases from Plants

<130> BC1019 US NA

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<151> 1999-09-21

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<211> 1388

<212> DNA

<213> Dimorphotheca

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<210> 2

<211> 287

<212> PRT

<213> Dimorphotheca

<400> 2

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      20              25              30

Ser Asp Thr Thr Gly Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr
      35              40              45

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Pro Ala Gly Leu Lys His Glu Leu Met Pro Lys His Val Ala Val Ile
 50 55 60
 Met Asp Gly Asn Arg Arg Trp Ala Arg Ser Arg Gly Leu Met Pro Asp
 65 70 75 80
 Ala Gly Tyr Met Glu Gly Ala Arg Ser Leu Lys Val Met Val Glu Leu
 85 90 95
 Cys Arg Lys Trp Gly Ile Gln Val Leu Thr Val Phe Ala Phe Ser Ala
 100 105 110
 Asp Asn Trp Leu Arg Pro Lys Val Glu Val Asp Phe Leu Met Gly Leu
 115 120 125
 Ile Glu Ser Val Leu Lys Asp Glu Val Val His Met Ile Lys Glu Gly
 130 135 140
 Ile Gln Leu Ser Val Ile Gly Asp Thr Ser Lys Leu Pro Lys Ser Val
 145 150 155 160
 Lys Arg Ile Ile Thr Tyr Ala Glu Asn Ile Thr Lys Asn Asn Ser Gln
 165 170 175
 Leu Asn Leu Val Val Ala Ile Asn Tyr Ser Gly Lys Tyr Asp Ile Val
 180 185 190
 Gln Ala Cys Gln Ser Ile Ala Leu Lys Val Lys Asp Gly Val Ile Gln
 195 200 205
 Pro Glu Glu Ile Asn Glu Phe Thr Ile Glu Asn Glu Leu Gly Thr Asn
 210 215 220
 Cys Ile Pro Phe Pro His Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
 225 230 235 240
 Leu Arg Val Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Thr Glu Leu
 245 250 255
 Tyr Phe Ser Glu Thr Leu Trp Pro Asp Phe Gly Glu Asp Glu Leu Leu
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 His Ala Leu Asn Thr Phe Gln His Arg Arg Arg Arg Tyr Gly Gly
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<210> 3

<211> 1082

<212> DNA

<213> Calendula officinalis

<400> 3

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gccatgagaa	agacgcttca	atctctcctt	tttcgatgtt	ccaaattcaa	aatcaaagcg	360
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<210> 4
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<212> PRT
<213> Calendula officinalis

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 1          5          10          15

Val Glu Lys Gly Trp Ser Pro Met Thr Gly His Ser Ala Met Arg Lys
          20          25          30

Thr Leu Gln Ser Leu Leu Phe Arg Cys Ser Lys Phe Lys Ile Lys Ala
          35          40          45

Val Ser Ile Tyr Ala Phe Ser Thr Glu Asn Trp Thr Arg Pro Lys Glu
          50          55          60

Glu Val Asp Phe Leu Met Glu Met Tyr Glu Asp Leu Leu Arg Thr Asp
          65          70          75          80

Ala Glu Glu Leu Leu Ser Leu Gly Cys Arg Val Ser Ile Met Gly Lys
          85          90          95

Lys Thr Asn Leu Pro Lys Ser Leu Gln Lys Leu Cys Ile Glu Ile Glu
          100          105          110

Glu Lys Ser Arg Ala Asn Ser Gly Thr His Val Asn Tyr Ala Leu Asn
          115          120          125

Tyr Ser Gly Lys Tyr Asp Ile Ile Glu Ala Cys Lys Ser Val Ala Thr
          130          135          140

Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
          145          150          155          160

Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
          165          170          175

Leu Val Ile Arg Thr Ser Gly Glu Ile Arg Leu Ser Asn Phe Met Leu
          180          185          190

Trp Gln Met Ala Tyr Ser Glu Leu Tyr Phe Thr Asp Lys Tyr Phe Pro
          195          200          205

Asp Phe Gly Glu Asn Asp Leu Ile Glu Ala Leu Leu Ala Phe Gln Lys
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Val Arg Lys Cys
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<211> 1071

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<212> DNA
<213> Hevea brasiliensis

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taagtcagtg atttaaggaa aatggaatta tacaacggtg agaggccaag tgtgttcaga 180
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gaaggaggtg gtcataaggc tggattttta gctcttctga acgtactaac ttattgctat 360
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aacttccaac gtcattattc ttacttggag aaacataagg aatacttaaa ataatttggt 1020
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<210> 6
<211> 290
<212> PRT
<213> Hevea brasiliensis

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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile
20 25 30
Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
35 40 45
Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
50 55 60
Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
65 70 75 80
Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
85 90 95
Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
100 105 110
Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
115 120 125
Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
130 135 140
Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
145 150 155 160
Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
165 170 175
Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
180 185 190

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
275 280 285

Leu Lys
290

<210> 7
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<212> DNA
<213> Hevea brasiliensis

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gaataaaact tgtagacctt gagaaaaaca cctacataaa tccttatacct gatgttctga 720
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<210> 8
<211> 290
<212> PRT
<213> Hevea brasiliensis

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20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys
35 40 45

Lys His Lys Leu Pro Glu Gly Gly His Lys Ala Gly Phe Leu Ala
50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala
 65 70 75 80
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
 85 90 95
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
 100 105 110
 Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
 115 120 125
 Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
 130 135 140
 Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
 145 150 155 160
 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
 165 170 175
 Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
 180 185 190
 Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
 195 200 205
 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
 210 215 220
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
 225 230 235 240
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
 260 265 270
 Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr
 275 280 285
 Leu Lys
 290

<210> 9

<211> 1000

<212> DNA

<213> Hevea brasiliensis

<400> 9

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<210> 10
 <211> 296
 <212> PRT
 <213> Hevea brasiliensis

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 Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys
 35 40 45
 Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala
 50 55 60
 Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val
 65 70 75 80
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu
 85 90 95
 Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile
 100 105 110
 Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val
 115 120 125
 Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys
 130 135 140
 Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala
 145 150 155 160
 Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser
 165 170 175
 Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu
 180 185 190
 Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile
 195 200 205
 Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu
 210 215 220
 Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr
 225 230 235 240
 Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn
 245 250 255
 Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg
 260 265 270
 His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu
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Glu Lys His Lys Glu Tyr Leu Lys
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<210> 11
<211> 1232
<212> DNA
<213> Vitis sp

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<210> 12
<211> 309
<212> PRT
<213> Vitis sp

<400> 12
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Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp
20 25 30
Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg
35 40 45
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn
50 55 60
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
65 70 75 80
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
85 90 95
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
100 105 110
Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
115 120 125

Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
130 135 140

Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
145 150 155 160

Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
165 170 175

Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
180 185 190

Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
195 200 205

Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
210 215 220

Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
225 230 235 240

Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
245 250 255

Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
260 265 270

Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
275 280 285

Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
290 295 300

Tyr Gly Gly Arg Asn
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<210> 13
<211> 1021
<212> DNA
<213> Oryza sativa

<400> 13
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ggctctgggc acaggggtggg cttctctgct ctcatggcca gcctgctcta ctgctatgaa 180
atgggcgtga agtatatcac ggtgtatgca tttagcatcg ataattttaa gcgagatccg 240
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agaaatgtca tcaacaagggt taactgtaag atcaacttct gggggaactt ggacatgttg 360
agcaaatacag tgagggtagc agctgagaaa ctgatggcta cactgctga aaacacggga 420
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<210> 14
 <211> 252
 <212> PRT
 <213> Oryza sativa

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 20 25 30
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 35 40 45
 Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
 50 55 60
 Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
 65 70 75 80
 Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
 85 90 95
 Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
 100 105 110
 Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
 115 120 125
 Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
 130 135 140
 Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
 145 150 155 160
 Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
 165 170 175
 Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
 180 185 190
 Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
 195 200 205
 Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
 210 215 220
 Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
 225 230 235 240
 Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 245 250

<210> 15
 <211> 900
 <212> DNA
 <213> Oryza sativa

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 gctgtcctct cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180

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cagagggagg atgctgacag tgttgcaaat aatgggtgtgt attcagacat ttcagtggca 660
gatctggacc gccatatgta cagcgtggtg tgccccgatc ctgacattgt gatccggacc 720
tcaggtgaga ctgcctgag caatttcctt ctgtggcaga cgacgttcag tcatttgcag 780
aatccagacc ctctttggcc ggagttctct ttcaagcacc ttgtctgggc catactccag 840
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<210> 16
 <211> 299
 <212> PRT
 <213> *Oryza sativa*

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Glu Asn Thr Asp Glu Leu Ile Ala Thr Gly Val Leu Ala Ser Leu Gln
          20             25             30

Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
      35             40             45

Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
      50             55             60

Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
      65             70             75             80

Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
          85             90             95

Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
      100             105             110

Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
      115             120             125

Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
      130             135             140

Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
      145             150             155             160

Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
          165             170             175

Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
      180             185             190

Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
      195             200             205

Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
      210             215             220

His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
      225             230             235             240

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Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe
245 250 255

Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys
260 265 270

His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile
275 280 285

Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
290 295

<210> 17
<211> 1028
<212> DNA
<213> Glycine max

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attctcacta ttatcactat cggtatcggt atcggttgta tcatcctttc catcaccggt 180
cccaaacaca gagtcttata gtctcgaagc gcggttcgac cattgcgaag tgtcacgctg 240
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cggcggaaact cgcggcggag atgatgccga agcatgtggc ggtgataatg gacgggaacg 360
ggaggtgggc gaaggtgaag gggctgccac catcggcggg gcaccaggcg ggggtgcaat 420
cgctgaggaa aatggtgagg ctgtgttgca gctggggaat taaggttcta acggttttcg 480
cgttctctac ggataactgg gttcgcccc aagtgagggt tgatttcttg atgaggctgt 540
ttgagagaac aataaactct gaagttcaaa cttttaagag ggaaggaatt agaatactctg 600
tgattggaga ttcatcaagg ttgcctgagt ctttaaaaag aatgatagct agtgcagaag 660
aggatacaaa acaaaattcg agattccaac ttattgtggc agtgggatac agtggaaaat 720
atgatgttgt gcaagcatgt aaaagtgtag ccaagaaagt caaagatggg cacattcact 780
tggatgacat aaacgaaaaac attattgaac aagaattgga aactaattgt actgagtttc 840
cttatcctga tctactaata cgaactagt ggcgagcttag agtgagtaac ttcttggtgt 900
ggcaattagc ctacacagaa ctttatttta atcgggaaact ctggccagat tttgggaagg 960
atgagtttgt agatgcatta agttcatttc aacaaagaca aagacgctat ggtgggtcgac 1020
attcataa 1028

<210> 18
<211> 322
<212> PRT
<213> Glycine max

<400> 18
Met Phe Ser Leu Arg Leu Pro Ile Pro Leu Val Lys Thr Pro Pro Ser
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Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
20 25 30

Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
35 40 45

Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
50 55 60

Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
65 70 75 80

Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
85 90 95

Met	Asp	Gly	Asn	Gly	Arg	Trp	Ala	Lys	Val	Lys	Gly	Leu	Pro	Pro	Ser	
			100					105					110			
Ala	Gly	His	Gln	Ala	Gly	Val	Gln	Ser	Leu	Arg	Lys	Met	Val	Arg	Leu	
		115					120					125				
Cys	Cys	Ser	Trp	Gly	Ile	Lys	Val	Leu	Thr	Val	Phe	Ala	Phe	Ser	Thr	
	130					135					140					
Asp	Asn	Trp	Val	Arg	Pro	Lys	Val	Glu	Val	Asp	Phe	Leu	Met	Arg	Leu	
145					150					155					160	
Phe	Glu	Arg	Thr	Ile	Asn	Ser	Glu	Val	Gln	Thr	Phe	Lys	Arg	Glu	Gly	
			165						170					175		
Ile	Arg	Ile	Ser	Val	Ile	Gly	Asp	Ser	Ser	Arg	Leu	Pro	Glu	Ser	Leu	
		180					185					190				
Lys	Arg	Met	Ile	Ala	Ser	Ala	Glu	Glu	Asp	Thr	Lys	Gln	Asn	Ser	Arg	
		195					200					205				
Phe	Gln	Leu	Ile	Val	Ala	Val	Gly	Tyr	Ser	Gly	Lys	Tyr	Asp	Val	Val	
	210					215					220					
Gln	Ala	Cys	Lys	Ser	Val	Ala	Lys	Lys	Val	Lys	Asp	Gly	His	Ile	His	
225					230					235					240	
Leu	Asp	Asp	Ile	Asn	Glu	Asn	Ile	Ile	Glu	Gln	Glu	Leu	Glu	Thr	Asn	
			245					250						255		
Cys	Thr	Glu	Phe	Pro	Tyr	Pro	Asp	Leu	Leu	Ile	Arg	Thr	Ser	Gly	Glu	
		260						265					270			
Leu	Arg	Val	Ser	Asn	Phe	Leu	Leu	Trp	Gln	Leu	Ala	Tyr	Thr	Glu	Leu	
		275				280					285					
Tyr	Phe	Asn	Arg	Glu	Leu	Trp	Pro	Asp	Phe	Gly	Lys	Asp	Glu	Phe	Val	
	290					295					300					
Asp	Ala	Leu	Ser	Ser	Phe	Gln	Gln	Arg	Gln	Arg	Arg	Tyr	Gly	Gly	Arg	
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His Ser

<210> 19

<211> 1026

<212> DNA

<213> Triticum aestivum

<400> 19

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gggaactcgc	ggtgggcggc	agcgcggggc	ctgccgccga	cggacgggca	cgagcacggg	180
atgcgcgcgc	tgatgaggac	ggtgcggctc	tcccgcgcct	ggggcatccg	cgtcctcacc	240
gccttcggtt	tctcgctcga	gaactggaat	cgccccaaag	cggaggttga	cttcttgatg	300
gccttgatcg	agaggtttat	caacgacaac	ctcgccgagt	tcttgaggga	agggacccgt	360
ctacgtataa	tcggtgaccg	ctcaaggctg	ccgatctctg	tgcagaagac	tgcacgagac	420
gccgaggagg	caacaagaaa	caactcgcag	ctcgatctag	tcctagccat	cagctacagc	480
ggcggaatgg	acattgtgca	ggcatgccgg	aatctcgccc	agaaagtgga	cgccaagctg	540
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gcccaatatc	tccaagccat	gatggccttc	cagagcagag	acaggcgctt	tggagaaga	780
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 aaaaaa 1026

<210> 20
 <211> 266
 <212> PRT
 <213> Triticum aestivum

<400> 20
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 20 25 30
 Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
 35 40 45
 Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
 50 55 60
 Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
 65 70 75 80
 Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
 85 90 95
 Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
 100 105 110
 Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
 115 120 125
 Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
 130 135 140
 Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
 145 150 155 160
 Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
 165 170 175
 Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
 180 185 190
 Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
 195 200 205
 Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
 210 215 220
 Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
 225 230 235 240
 Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
 245 250 255
 Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu
 260 265

<210> 21
 <211> 11

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Domain I of
 published alignment

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 <223> X = any amino acid

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 <222> (8)
 <223> X = any amino acid

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 <222> (10)
 <223> X = any amino acid

 <300>
 <301> Apfel, C. M.
 <302> Use of Genomincs to Indentify Bacterial Undecaprenyl
 Pyrophosphate Synthetase: Clooning, Expression, and
 Characterization of the Essential uppS Gene
 <303> J. Bacteriol.
 <304> 81
 <306> 483-492
 <307> 1999

 <400> 21
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 1 5 10

 <210> 22
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Domain V of published
 alignment

 <220>
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 <222> (3)
 <223> X = any amino acid

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 Leu Trp Gln Xaa Xaa Tyr Xaa Glu
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<210> 23
 <211> 750
 <212> DNA
 <213> Micrococcus luteus

<300>
 <301> Shimizu, N.
 <302> Molecular Cloning, Expression, and Purification of Undecprenyl
 Diphosphate Synthase: No Sequence Similarity between E- and
 Z-prenyl Diphosphate Synthases
 <303> J. Biol. Chem.
 <304> 273
 <306> 19476-19481
 <307> 1998

<400> 23
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 gaagaacgtt taagtaactt ttttaatttg caatgttcat atagtgaagt tgtatttata 660
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<210> 24
 <211> 249
 <212> PRT
 <213> Micrococcus luteus

<400> 24
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 Ala Ala Gln Ile Pro Lys His Ile Ala Ile Ile Met Asp Gly Asn Gly
 20 25 30
 Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu
 35 40 45
 Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly
 50 55 60
 Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg
 65 70 75 80

<400> 26
 Met Glu Thr Asp Ser Gly Ile Pro Gly His Ser Phe Val Leu Lys Trp
 1 5 10 15
 Thr Lys Asn Ile Phe Ser Arg Thr Leu Arg Ala Ser Asn Cys Val Pro
 20 25 30
 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys
 35 40 45
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met
 50 55 60
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr
 65 70 75 80
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val
 85 90 95
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu
 100 105 110
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly
 115 120 125
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala
 130 135 140
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe
 145 150 155 160
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile
 165 170 175
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
 180 185 190
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
 195 200 205
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
 210 215 220
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
 225 230 235 240
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
 245 250 255
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
 260 265 270
 Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn
 275 280 285

<210> 27
 <211> 1032
 <212> DNA
 <213> *Saccharomyces cerevisiae*
 <300>
 <308> AB013498

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tcaccaagga ttaatatag aaattttact aataaaatgt acatgggttt ccattccaat 720
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caagtacatg aaaatgccac cattgaattt agtgatacgt tgtggccaaa ttttagcttc 840
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gagaagaatc actcattggt tgaaaaaata catgaaagcg ttccttcaat atttaaaaaa 960
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ggagatgaat aa 1032

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<210> 28

<211> 343

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 28

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      20              25              30

Phe Gln Arg Val Phe Ala Trp Val Met Ser Leu Ser Leu Phe Ser Trp
      35              40              45

Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly
      50              55              60

Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr
      65              70              75              80

Ala Lys Ser Arg Arg Leu Pro Val Lys Lys Gly His Glu Ala Gly Gly
      85              90              95

Leu Thr Leu Leu Thr Leu Leu Tyr Ile Cys Lys Arg Leu Gly Val Lys
      100             105             110

Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys
      115             120             125

Glu Glu Val Asp Thr Leu Met Asn Leu Phe Thr Val Lys Leu Asp Glu
      130             135             140

Phe Ala Lys Arg Ala Lys Asp Tyr Lys Asp Pro Leu Tyr Gly Ser Lys
      145             150             155             160

Ile Arg Ile Val Gly Asp Gln Ser Leu Leu Ser Pro Glu Met Arg Lys
      165             170             175

Lys Ile Lys Lys Val Glu Glu Ile Thr Gln Asp Gly Asp Asp Phe Thr
      180             185             190

Leu Phe Ile Cys Phe Pro Tyr Thr Ser Arg Asn Asp Met Leu His Thr
      195             200             205

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Ile Arg Asp Ser Val Glu Asp His Leu Glu Asn Lys Ser Pro Arg Ile
 210 215 220
 Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn
 225 230 235 240
 Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp
 245 250 255
 Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp
 260 265 270
 Thr Leu Trp Pro Asn Phe Ser Phe Phe Ala Met Tyr Leu Met Ile Leu
 275 280 285
 Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His
 290 295 300
 Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys
 305 310 315 320
 Lys Lys Thr Ala Met Ser Leu Tyr Asn Phe Pro Asn Pro Pro Ile Ser
 325 330 335
 Val Ser Val Thr Gly Asp Glu
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<210> 29
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 29
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32

<210> 30
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 30
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36

<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 31
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26

<210> 32
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 32
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 <210> 33
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 33
 acggatccat gttctcgta agactcc 27

 <210> 34
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 34
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 <210> 35
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

 <400> 35
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 <210> 36
 <211> 34
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:primer

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 <210> 37
 <211> 1200

<212> DNA
 <213> arabidopsis

<400> 37
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 aagtgtgttc tttaaattatc ttctctgata accaaaaaag ccctattttc cgagatgaat 240
 accctagaag aagtagatga atccactcat atcttcaacg ctttgatgag tctaatagagg 300
 aaatttttgt tcagagttct atgcgctcggc ccaatcccta ctaacatttc attcatcatg 360
 gatggaaacc gcaggttcgc taagaaacac aatcttatag gcctagatgc aggacataga 420
 gctggtttca tatccgtgaa atatattctt caatactgca aagagattgg tgtaccgtac 480
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